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Sequence Listing was accepted.

See attached Validation Report.

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Reviewer: markspencer

Timestamp: [year=2009; month=6; day=26; hr=9; min=43; sec=18; ms=727;]

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Application No: 10554625 Version No: 1.0

Input Set:**Output Set:**

Started: 2009-06-11 15:50:53.475
Finished: 2009-06-11 15:50:54.066
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 591 ms
Total Warnings: 2
Total Errors: 18
No. of SeqIDs Defined: 2
Actual SeqID Count: 2

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
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E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (2)

SEQUENCE LISTING

<110> CHIRON CORPORATION

<120> COMPOSITIONS COMPRISING CATIONIC MICROPARTICLES
AND HCV E1E2 DNA AND METHODS OF USE THEREOF

<130> 2300-20407.40 (PP20407.003)

<140> 10554625

<141> 2009-06-11

<150> PCT/US2004/012510

<151> 2004-04-23

<150> 60/465,841

<151> 2003-04-25

<160> 2

<170> PatentIn Ver. 2.0

<210> 1

<211> 1914

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HCV-1 E1/E2/p7 region

<220>

<221> CDS

<222> (1)..(1911)

<400> 1

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1 5 10 15	

gct tcg gcc tac caa gtg cgc aac tcc acg ggg ctc tac cac gtc acc	96
Ala Ser Ala Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr	
20 25 30	

aat gat tgc cct aac tcg agt att gtg tac gag gcg gcc gat gcc atc	144
Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile	
35 40 45	

ctg cac act ccg ggg tgc gtc cct tgc gtt cgc gag ggc aac gcc tcg	192
Leu His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser	
50 55 60	

agg tgt tgg gtg gcg atg acc cct acg gtg gcc acc agg gat ggc aaa	240
Arg Cys Trp Val Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys	
65 70 75 80	

ctc ccc gcg acg cag ctt cga cgt cac atc gat ctg ctt gtc ggg agc	288
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Leu	Pro	Ala	Thr	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val	Gly	Ser		
				85					90					95			
gcc	acc	ctc	tgt	tcg	gcc	ctc	tac	gtg	ggg	gac	ctg	tgc	ggg	tct	gtc	336	
Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys	Gly	Ser	Val		
			100					105					110				
ttt	ctt	gtc	ggc	caa	ctg	ttt	acc	ttc	tct	ccc	agg	cgc	cac	tgg	acg	384	
Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	Arg	His	Trp	Thr		
			115					120					125				
acg	caa	ggg	tgc	aat	tgc	tct	atc	tat	ccc	ggc	cat	ata	acg	ggg	cac	432	
Thr	Gln	Gly	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His		
			130					135				140					
cgc	atg	gca	tgg	gat	atg	atg	atg	aac	tgg	tcc	cct	acg	acg	gcg	ttg	480	
Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu		
					145			150			155				160		
gta	atg	gct	cag	ctg	ctc	cgg	atc	cca	caa	gcc	atc	ttg	gac	atg	atc	528	
Val	Met	Ala	Gln	Leu	Leu	Arg	Ile	Pro	Gln	Ala	Ile	Leu	Asp	Met	Ile		
				165				170					175				
gct	ggg	gct	cac	tgg	gga	gtc	ctg	gcg	ggc	ata	gcg	tat	ttc	tcc	atg	576	
Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met		
			180					185					190				
gtg	ggg	aac	tgg	gcg	aag	gtc	ctg	gta	gtg	ctg	ctg	cta	ttt	gcc	ggc	624	
Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Val	Val	Leu	Leu	Leu	Phe	Ala	Gly		
			195					200				205					
gtc	gac	gcg	gaa	acc	cac	gtc	acc	ggg	gga	agt	gcc	ggc	cac	act	gtg	672	
Val	Asp	Ala	Glu	Thr	His	Val	Thr	Gly	Gly	Ser	Ala	Gly	His	Thr	Val		
			210					215				220					
tct	gga	ttt	gtt	agc	ctc	ctc	gca	cca	ggc	gcc	aag	cag	aac	gtc	cag	720	
Ser	Gly	Phe	Val	Ser	Leu	Leu	Ala	Pro	Gly	Ala	Lys	Gln	Asn	Val	Gln		
					225			230				235			240		
ctg	atc	aac	acc	aac	ggc	agt	tgg	cac	ctc	aat	agc	acg	gcc	ctg	aac	768	
Leu	Ile	Asn	Thr	Asn	Gly	Ser	Trp	His	Leu	Asn	Ser	Thr	Ala	Leu	Asn		
				245				250					255				
tgc	aat	gat	agc	ctc	aac	acc	ggc	tgg	ttg	gca	ggg	ctt	ttc	tat	cac	816	
Cys	Asn	Asp	Ser	Leu	Asn	Thr	Gly	Trp	Leu	Ala	Gly	Leu	Phe	Tyr	His		
				260				265					270				
cac	aag	ttc	aac	tct	tca	ggc	tgt	cct	gag	agg	cta	gcc	agc	tgc	cga	864	
His	Lys	Phe	Asn	Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	Cys	Arg		
			275					280				285					
ccc	ctt	acc	gat	ttt	gac	cag	ggc	tgg	ggc	cct	atc	agt	tat	gcc	aac	912	
Pro	Leu	Thr	Asp	Phe	Asp	Gln	Gly	Trp	Gly	Pro	Ile	Ser	Tyr	Ala	Asn		
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gga	agc	ggc	ccc	gac	cag	cgc	ccc	tac	tgc	tgg	cac	tac	ccc	cca	aaa	960	

Gly	Ser	Gly	Pro	Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Pro	Pro	Lys	
305					310					315					320	
cct	tgc	ggc	att	gtg	ccc	gcg	aag	agt	gtg	tgt	ggc	ccg	gta	tat	tgc	1008
Pro	Cys	Gly	Ile	Val	Pro	Ala	Lys	Ser	Val	Cys	Gly	Pro	Val	Tyr	Cys	
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ttc	act	ccc	agc	ccc	gtg	gtg	gtg	gga	acg	acc	gac	agg	tcg	ggc	gcg	1056
Phe	Thr	Pro	Ser	Pro	Val	Val	Val	Gly	Thr	Thr	Asp	Arg	Ser	Gly	Ala	
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ccc	acc	tac	agc	tgg	ggc	gaa	aat	gat	acg	gac	gtc	ttc	gtc	ctt	aac	1104
Pro	Thr	Tyr	Ser	Trp	Gly	Glu	Asn	Asp	Thr	Asp	Val	Phe	Val	Leu	Asn	
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aat	acc	agg	cca	ccg	ctg	ggc	aat	tgg	ttc	ggc	tgt	acc	tgg	atg	aac	1152
Asn	Thr	Arg	Pro	Pro	Leu	Gly	Asn	Trp	Phe	Gly	Cys	Thr	Trp	Met	Asn	
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tca	act	gga	ttc	acc	aaa	gtg	tgc	gga	gcg	cct	cct	tgt	gtc	atc	gga	1200
Ser	Thr	Gly	Phe	Thr	Lys	Val	Cys	Gly	Ala	Pro	Pro	Cys	Val	Ile	Gly	
385					390					395					400	
ggg	gcg	ggc	aac	aac	acc	ctg	cac	tgc	ccc	act	gat	tgc	ttc	cgc	aag	1248
Gly	Ala	Gly	Asn	Asn	Thr	Leu	His	Cys	Pro	Thr	Asp	Cys	Phe	Arg	Lys	
			405					410					415			
cat	ccg	gac	gcc	aca	tac	tct	cgg	tgc	ggc	tcc	ggc	ccc	tgg	atc	aca	1296
His	Pro	Asp	Ala	Thr	Tyr	Ser	Arg	Cys	Gly	Ser	Gly	Pro	Trp	Ile	Thr	
			420					425					430			
ccc	agg	tgc	ctg	gtc	gac	tac	ccg	tat	agg	ctt	tgg	cat	tat	cct	tgt	1344
Pro	Arg	Cys	Leu	Val	Asp	Tyr	Pro	Tyr	Arg	Leu	Trp	His	Tyr	Pro	Cys	
		435					440					445				
acc	atc	aac	tac	act	ata	ttt	aaa	atc	agg	atg	tac	gtg	gga	ggg	gtc	1392
Thr	Ile	Asn	Tyr	Thr	Ile	Phe	Lys	Ile	Arg	Met	Tyr	Val	Gly	Gly	Val	
	450					455					460					
gag	cac	agg	ctg	gaa	gct	gcc	tgc	aac	tgg	acg	cgg	ggc	gaa	cgt	tgc	1440
Glu	His	Arg	Leu	Glu	Ala	Ala	Cys	Asn	Trp	Thr	Arg	Gly	Glu	Arg	Cys	
465					470				475					480		
gat	ctg	gaa	gat	agg	gac	agg	tcc	gag	ctc	agc	ccg	tta	ctg	ctg	acc	1488
Asp	Leu	Glu	Asp	Arg	Asp	Arg	Ser	Glu	Leu	Ser	Pro	Leu	Leu	Leu	Thr	
			485					490					495			
act	aca	cag	tgg	cag	gtc	ctc	ccg	tgt	tcc	ttc	aca	acc	ctg	cca	gcc	1536
Thr	Thr	Gln	Trp	Gln	Val	Leu	Pro	Cys	Ser	Phe	Thr	Thr	Leu	Pro	Ala	
		500						505					510			
ttg	tcc	acc	ggc	ctc	atc	cac	ctc	cac	cag	aac	att	gtg	gac	gtg	cag	1584
Leu	Ser	Thr	Gly	Leu	Ile	His	Leu	His	Gln	Asn	Ile	Val	Asp	Val	Gln	
		515					520					525				
tac	ttg	tac	ggg	gtg	ggg	tca	agc	atc	gcg	tcc	tgg	gcc	att	aag	tgg	1632
Tyr	Leu	Tyr	Gly	Val	Gly	Ser	Ser	Ile	Ala	Ser	Trp	Ala	Ile	Lys	Trp	

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gag tac gtc gtc ctc ctg ttc ctt ctg ctt gca gac gcg cgc gtc tgc			1680
Glu Tyr Val Val Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Val Cys			
545	550	555	560
tcc tgc ttg tgg atg atg cta ctc ata tcc caa gcg gaa gcg gct ttg			1728
Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu Ala Ala Leu			
	565	570	575
gag aac ctc gta ata ctt aat gca gca tcc ctg gcc ggg acg cac ggt			1776
Glu Asn Leu Val Ile Leu Asn Ala Ala Ser Leu Ala Gly Thr His Gly			
	580	585	590
ctt gta tcc ttc ctc gtg ttc ttc tgc ttt gca tgg tat ctg aag ggt			1824
Leu Val Ser Phe Leu Val Phe Phe Cys Phe Ala Trp Tyr Leu Lys Gly			
	595	600	605
aag tgg gtg ccc gga gcg gtc tac acc ttc tac ggg atg tgg cct ctc			1872
Lys Trp Val Pro Gly Ala Val Tyr Thr Phe Tyr Gly Met Trp Pro Leu			
	610	615	620
ctc ctg ctc ctg ttg gcg ttg ccc cag cgg gcg tac gcg taa			1914
Leu Leu Leu Leu Leu Ala Leu Pro Gln Arg Ala Tyr Ala			
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<210> 2

<211> 637

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HCV-1 E1/E2/p7 region

<400> 2

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Ala Ser Ala Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr
20 25 30

Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile
35 40 45

Leu His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser
50 55 60

Arg Cys Trp Val Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys
65 70 75 80

Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser
85 90 95

Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Ser Val
100 105 110

Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	Arg	His	Trp	Thr	115	120	125
Thr	Gln	Gly	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His	130	135	140
Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	145	150	155
Val	Met	Ala	Gln	Leu	Leu	Arg	Ile	Pro	Gln	Ala	Ile	Leu	Asp	Met	Ile	165	170	175
Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met	180	185	190
Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Val	Val	Leu	Leu	Leu	Phe	Ala	Gly	195	200	205
Val	Asp	Ala	Glu	Thr	His	Val	Thr	Gly	Gly	Ser	Ala	Gly	His	Thr	Val	210	215	220
Ser	Gly	Phe	Val	Ser	Leu	Leu	Ala	Pro	Gly	Ala	Lys	Gln	Asn	Val	Gln	225	230	235
Leu	Ile	Asn	Thr	Asn	Gly	Ser	Trp	His	Leu	Asn	Ser	Thr	Ala	Leu	Asn	245	250	255
Cys	Asn	Asp	Ser	Leu	Asn	Thr	Gly	Trp	Leu	Ala	Gly	Leu	Phe	Tyr	His	260	265	270
His	Lys	Phe	Asn	Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	Cys	Arg	275	280	285
Pro	Leu	Thr	Asp	Phe	Asp	Gln	Gly	Trp	Gly	Pro	Ile	Ser	Tyr	Ala	Asn	290	295	300
Gly	Ser	Gly	Pro	Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Pro	Pro	Lys	305	310	315
Pro	Cys	Gly	Ile	Val	Pro	Ala	Lys	Ser	Val	Cys	Gly	Pro	Val	Tyr	Cys	325	330	335
Phe	Thr	Pro	Ser	Pro	Val	Val	Val	Gly	Thr	Thr	Asp	Arg	Ser	Gly	Ala	340	345	350
Pro	Thr	Tyr	Ser	Trp	Gly	Glu	Asn	Asp	Thr	Asp	Val	Phe	Val	Leu	Asn	355	360	365
Asn	Thr	Arg	Pro	Pro	Leu	Gly	Asn	Trp	Phe	Gly	Cys	Thr	Trp	Met	Asn	370	375	380
Ser	Thr	Gly	Phe	Thr	Lys	Val	Cys	Gly	Ala	Pro	Pro	Cys	Val	Ile	Gly	385	390	395
Gly	Ala	Gly	Asn	Asn	Thr	Leu	His	Cys	Pro	Thr	Asp	Cys	Phe	Arg	Lys	405	410	415

His	Pro	Asp	Ala	Thr	Tyr	Ser	Arg	Cys	Gly	Ser	Gly	Pro	Trp	Ile	Thr	420	425	430	
Pro	Arg	Cys	Leu	Val	Asp	Tyr	Pro	Tyr	Arg	Leu	Trp	His	Tyr	Pro	Cys	435	440	445	
Thr	Ile	Asn	Tyr	Thr	Ile	Phe	Lys	Ile	Arg	Met	Tyr	Val	Gly	Gly	Val	450	455	460	
Glu	His	Arg	Leu	Glu	Ala	Ala	Cys	Asn	Trp	Thr	Arg	Gly	Glu	Arg	Cys	465	470	475	480
Asp	Leu	Glu	Asp	Arg	Asp	Arg	Ser	Glu	Leu	Ser	Pro	Leu	Leu	Leu	Thr	485	490	495	
Thr	Thr	Gln	Trp	Gln	Val	Leu	Pro	Cys	Ser	Phe	Thr	Thr	Leu	Pro	Ala	500	505	510	
Leu	Ser	Thr	Gly	Leu	Ile	His	Leu	His	Gln	Asn	Ile	Val	Asp	Val	Gln	515	520	525	
Tyr	Leu	Tyr	Gly	Val	Gly	Ser	Ser	Ile	Ala	Ser	Trp	Ala	Ile	Lys	Trp	530	535	540	
Glu	Tyr	Val	Val	Leu	Leu	Phe	Leu	Leu	Leu	Ala	Asp	Ala	Arg	Val	Cys	545	550	555	560
Ser	Cys	Leu	Trp	Met	Met	Leu	Leu	Ile	Ser	Gln	Ala	Glu	Ala	Ala	Leu	565	570	575	
Glu	Asn	Leu	Val	Ile	Leu	Asn	Ala	Ala	Ser	Leu	Ala	Gly	Thr	His	Gly	580	585	590	
Leu	Val	Ser	Phe	Leu	Val	Phe	Phe	Cys	Phe	Ala	Trp	Tyr	Leu	Lys	Gly	595	600	605	
Lys	Trp	Val	Pro	Gly	Ala	Val	Tyr	Thr	Phe	Tyr	Gly	Met	Trp	Pro	Leu	610	615	620	
Leu	Leu	Leu	Leu	Leu	Ala	Leu	Pro	Gln	Arg	Ala	Tyr	Ala				625	630	635	